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OM nucleic - nucleic search, using SW model

Run on: June 6, 2006, 17:51:08 ; Search time 3466.43 Seconds
(without alignments)

10607.392 Million cell updates/sec

Title: US-10-698-160-1

Perfect score: 575

Sequence: 1 tcaggcagtgtcaggag.....gcggaaaagggtgtggctgt 575

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0⁺, Maximum Match 100⁺

Listing first 45 summaries

Database : GenBnbl:*

1: 9b_env:*

2: 9b_pat:*

3: 9b_ph:*

4: 9b_pl:*

5: 9b_pr:*

6: 9b_ro:*

7: 9b_sts:*

8: 9b_sy:*

9: 9b_un:*

10: 9b_v1:*

11: 9b_vor:*

12: 9b_htg:*

13: 9b_in:*

14: 9b_om:*

15: 9b_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1	575	100.0	171823	10	HRV507799	AJ507799 Human her
2	575	100.0	172281	10	EBV	V01555 Epstein-Bar
3	575	100.0	184113	10	HS4B958BAJ	M80517 Epstein-Bar
C 4	536.6	93.3	3060	10	HS4LMP	M28682 Epstein-Bar
C 5	504.6	87.8	171657	10	AY961628	AY961628 Human her
C 6	498.2	86.6	2038	10	HBNLFL	X58140 Human nasop
C 7	498.2	86.6	2038	10	HS4LMP1	D11059 Human herpe
C 8	484.2	84.2	3407	10	HSAMP	K02165 Epstein-Bar
C 9	464.8	80.8	1009	10	HRU86104	U66104 Human herpe
C 10	451.2	78.5	2031	10	EBVLMPI	X66863 Epstein-Bar
C 11	451.2	78.5	2031	10	HS4LMPB	M83720 Epstein-Bar
C 12	428	74.4	515	10	HRE278757	AJ278797 Human her
C 13	428	74.4	515	10	HRE278798	AJ278798 Human her
C 14	405.6	70.5	515	10	HRE278794	AJ278794 Human her
C 15	405.6	70.5	515	10	HHE278795	AJ278795 Human her
C 16	404	70.3	515	10	HHE278796	AJ278796 Human her
C 17	368.8	64.1	406	10	BEA1676	AJ001676 Epstein-B
C 18	202.4	35.2	204	10	EBVLMPI228	X81784 Epstein-Bar

ALIGNMENTS

RESULT 1

HRV507799

LOCUS Human herpesvirus 4 complete wild type genome.

DEFINITION Human herpesvirus 4

ACCESSION AJ507799

VERSION AJ507799.2

KEYWORDS GI:86261677

SOURCE Human herpesvirus 4 (Epstein-Barr virus)

ORGANISM Human herpesvirus 4

Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Lymphocryptovirus.

REFERENCE 1

Arrand, J.R., Rymo, L., Walsh, J.E., Bjork, E., Lindahl, T. and Griffin, B.E.

TITLE Molecular cloning of the complete Epstein-Barr virus genome as a set of overlapping restriction endonuclease fragments

JOURNAL Nucleic Acids Res. 9 (13), 2999-3014 (1981)

PUBMED 6265068

REFERENCE 2

AUTHORS Kozak, M.

TITLE Possible role of flanking nucleotides in recognition of the AUG initiator codon by eukaryotic ribosomes

JOURNAL Nucleic Acids Res. 9 (20), 5233-5252 (1981)

PUBMED 7301588

REFERENCE 3

AUTHORS Deininger, P.L., Bankier, A., Farrell, P., Baer, R., and Barrell, B.

TITLE Sequence analysis and in vitro transcription of portions of the Epstein-Barr virus genome

JOURNAL J. Cell. Biochem. 19 (3), 267-274 (1982)

PUBMED 6296170

REFERENCE 4

AUTHORS Farrell, P.J., Bankier, A., Seguin, C., Deininger, P., and Barrell, B.G.

TITLE Latent and lytic cycle promoters of Epstein-Barr virus

JOURNAL EMBO J. 2 (8), 1331-1338 (1983)

PUBMED 10872327

REFERENCE 5

AUTHORS Farrell, P.J., Deininger, P.L., Bankier, A., and Barrell, B.

TITLE Homologous upstream sequences near Epstein-Barr virus promoters

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 80 (6), 1565-1569 (1983)

PUBMED 6300857

REFERENCE 6

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	575	100.0	1177	12	ADO43140			Ado43140 Epstein-B
2	575	100.0	172281	12	ADN12151			Adn12151 Epstein-B
C	3	451.2	78.5	2031	12	ADN12158		Aaz17263 Human gen
C	4	69.2	12.0	1337	2	AAZ17263		Adc86736 Human GPC
C	5	68.2	11.9	5452	10	ADC86736		Adc867060 Human GPC
C	6	67.6	11.8	3163	10	ADC87060		Adc6733 Human GPC
C	7	67.4	11.7	3133	10	ADC86738		Acn54594 Coton an
C	8	66.8	11.6	629	13	ACN54594		Abk98631 Vector PE
C	9	66.8	11.6	12733	6	ABK98631		Adc13882 L. lactis
C	10	66.8	11.6	12733	9	ACD13882		Abk98592 Vector PE
C	11	66.8	11.6	12739	6	ABK98592		Acd13843 Plasmid p
C	12	66.8	11.6	12739	9	ACD13843		Acn54596 Coton an
C	13	63.6	11.1	598	13	ACN54596		Adc86688 Human GPC
C	14	63.6	11.1	1117	10	ADC86688		Abt09682 Human PAL
C	15	62.6	10.9	1065	6	ABT09682		Aaa02484 Human col
C	16	62	10.8	1000	3	AAA02484		Abg37080 Mouse pla
C	17	61.6	10.7	2898	10	ADG37080		Abt09678 Human PAL
C	18	61	10.6	1064	6	ABT09678		

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OM nucleic - nucleic search, using sw modal

Run on: June 6, 2006, 17:52:13 ; Search time 3888.44 Seconds
(without alignments)

2699.032 Million cell updates/sec

Title: US-10-698-160-1
Perfect score: 575
Sequence: 1 tcaggcgtgtcaggag.....gcggaaaagggtgtggctgt 575

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

```

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est3:*
9: gb_est4:*
10: gb_est9:*
11: gb_g8a1:*
12: gb_g8a2:*
13: gb_g8a3:*
14: gb_g8a4:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	85	14.8	1421	9	DN653570	DN653570 CEC06-C08	
2	81.8	14.2	817	9	DN898203	DN898203 74134031	
3	81.8	14.2	1607	19	DT779627	DV779627 Hw Fat 35	
c 4	81.6	14.2	1129	12	CL045106	CL045106 CH216-72B	
c 5	81.6	14.2	1301	14	AG63665	AG63665 Mus musculus	
c 6	81.6	14.2	1560	12	CL081488	CL081488 CH216-162	
c 7	81.6	14.2	1593	12	CC255263	CC255263 CH216-42A	
c 8	81.4	14.2	1021	3	BO41712	BO41712 AGENCOURT	
c 9	81	14.1	1287	13	CW948789	CW948789 TCB33.1 H	
10	80.8	14.1	774	7	BE040676	BE040676 OPO4H04_O	
11	80.8	14.1	849	4	CB905469	CB905469 tric074xk	
12	80.8	14.1	849	5	CF876976	CF876976 tric074xk	
13	80.6	14.0	1591	12	CL077232	CL077232 CH216-143	
14	80.6	14.0	1738	12	CG750956	CG750956 P045-2-H0	
15	80.4	14.0	956	13	CW951178	CW951178 TCB36.3_D	
c 16	80.4	14.0	1362	3	BM55092	BM55092 AGENCOURT	
c 17	80.2	13.9	1471	10	DV781271	DV781271 Hw Fat 35	
c 18	80	13.9	1099	13	CL509275	CL509275 SATL81	
c 19	80	13.9	1201	12	CL082769	CL082769 CH216-171	

ALIGNMENTS

RESULT 1
DN653570
LOCUS CEC06-C08.xid-t
DEFINITION SHGC-CBC Gasterosteus aculeatus cDNA clone
CBO6-C08 3', mRNA sequence.
ACCESSION DN653570
KEYWORDS EST.
SOURCE Gasterosteus aculeatus (three spined stickleback)
ORGANISM Gasterosteidae; Actinopterygii; Neopterygi; Teleostei; Euteleostomi; Acanthomorpha; Acanthopterygii; Percormorpha; Gasterosteiformes; Gasterosteidae; Gasterosteus.
TAXON 1 (bases 1 to 1421)
AUTHORS Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M., Schmitz,J., and Myers,R.M.
TITLE Unpublished sequence tags from *Gasterosteus aculeatus*
JOURNAL Unpublished (2003)
COMMENT Contact: Grimwood, Jane
STANFORD HUMAN GENOME CENTER
975 S CALIFORNIA AVE, PALO ALTO, CA 94304, USA
TEL: 650 320 5917
FAX: 650 320 5801
EMAIL: Jane@hgsc.stanford.edu
PLATE: 06
HIGH QUALITY SEQUENCE START: 4
HIGH QUALITY SEQUENCE STOP: 347.
LOCATION/QUALIFIERS
1. .1421
/organism="Gasterosteus aculeatus"
/mol_type="mRNA"
/strain="Conner Creek sticklebacks, WA USA"
/db_xref="taxon:69293"
/clone="CBO6-C08"
/sex="mixed male and female"
/tissue_type="skin"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="SHGC-CBC"
/note="vector: Express 1; total and poly A+ RNA was

Post-processing: Minimum Match 0% Maximum Match 100%									
Listing first 45 summaries									
Database : Issued Patents_NA:*									
1: /EMC_Celerra_SIDSS3/prodata/2/ina/1 COMB. seq:*									
2: /EMC_Celerra_SIDSS3/prodata/2/ina/5 COMB. seq:*									
3: /EMC_Celerra_SIDSS3/prodata/2/ina/6 COMB. seq:*									
4: /EMC_Celerra_SIDSS3/prodata/2/ina/7 COMB. seq:*									
5: /EMC_Celerra_SIDSS3/prodata/2/ina/R COMB. seq:*									
6: /EMC_Celerra_SIDSS3/prodata/2/ina/PP COMB. seq:*									
7: /EMC_Celerra_SIDSS3/prodata/2/ina/PP COMB. seq:*									
8: /EMC_Celerra_SIDSS3/prodata/2/ina/RS COMB. seq:*									
9: /EMC_Celerra_SIDSS3/prodata/2/ina/backfile1.seq:*									
10: /EMC_Celerra_SIDSS3/prodata/2/ina/backfile1.seq:*									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution:									
SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description				
c 1	86.4	15.0	7218	2	US-08-232-463-14	Sequence 14, Appl			
c 2	69.2	12.0	1337	4	US-09-297-648-4735	Sequence 4735, Appl			
c 3	54.4	9.5	53526	3	US-08-638-136-1	Sequence 2, Appl			
c 4	54.4	9.5	53577	3	US-08-638-136-1	Sequence 1, Appl			
c 5	54.4	9.5	53577	3	US-08-460-215A-1	Sequence 1, Appl			
c 6	53.4	9.3	9293	3	US-09-949-016-16801	Sequence 16801, Appl			
c 7	53.4	9.3	767677	3	US-09-949-016-12147	Sequence 12147, Appl			
c 8	53.4	9.3	767677	3	US-09-949-016-17361	Sequence 17361, Appl			
c 9	52.8	9.2	18855	3	US-09-949-016-13343	Sequence 13343, Appl			
c 10	52.8	9.2	30678	3	US-09-949-016-12818	Sequence 12818, Appl			
c 11	51.52	9.0	320	3	US-09-165-263-11	Sequence 11, Appl			
c 12	51.8	9.0	1454	4	US-09-297-648-4508	Sequence 4508, Appl			
c 13	51.2	8.9	320	3	US-09-165-264-14	Sequence 14, Appl			
c 14	50	8.7	50	2	US-08-171-389-558	Sequence 558, Appl			
c 15	50	8.7	50	2	US-08-123-936-558	Sequence 558, Appl			
c 16	50	8.7	50	2	US-08-175-222A-558	Sequence 558, Appl			
c 17	50	8.7	50	3	US-08-482-080A-558	Sequence 558, Appl			
c 18	50	8.7	50	3	US-09-354-947-558	Sequence 558, Appl			
c 19	50	8.7	50	3	US-09-933-346-558	Sequence 558, Appl			
c 20	49.8	8.7	50	7	PCT-US91-12368-558	Sequence 558, Appl			
c 21	49.8	8.7	289	3	US-09-007-005-17	Sequence 17, Appl			
c 22	49.8	8.7	289	3	US-09-244-796-17	Sequence 17, Appl			
c 23	49.8	8.7	320	3	US-09-165-264-13	Sequence 13, Appl			

GenCore version 5.1.9
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Run on: June 6, 2006, 18:40:59 ; Search time 37.9911 Seconds
 (without alignments)
 1782.525 Million cell updates/sec

Title: US-10-698-160-1
 perfect score: 575
 Sequence: 1 tcagggcagtgtcaggaa.....gcgaaaagggtgggtgt 575

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 246837 seqs, 5888690 residues

total number of hits satisfying chosen parameters: 493674

minimum DD seq length: 0
 maximum DD seq length: 0
 minimum DB seq length: 0
 maximum DB seq length: 0

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries						
Database :	Query	Match	Length	DB	ID	Description
result	No.	Score	Score	Length	DB	ID
1 :	Published Applications NA New					
1 :	/EMC_Celerra_SID33/ptodata2/pubpna/US09_NEW_PUB.seq:*					
2 :	/EMC_Celerra_SID33/ptodata2/pubpna/US06_NEW_PUB.seq:*					
3 :	/EMC_Celerra_SID33/ptodata2/pubpna/US07_NEW_PUB.seq:*					
4 :	/EMC_Celerra_SID33/ptodata2/pubpna/US08_NEW_PUB.seq:*					
5 :	/EMC_Celerra_SID33/ptodata2/pubpna/US10_NEW_PUB.seq:*					
6 :	/EMC_Celerra_SID33/ptodata2/pubpna/US11_NEW_PUB.seq:*					
7 :	/EMC_Celerra_SID33/ptodata2/pubpna/US60_NEW_PUB.seq:*					
8 :	/EMC_Celerra_SID33/ptodata2/pubpna/US60_NEW_PUB.seq:*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
1	41.4	7.2	1682	6	US-0-953-349-31197	Sequence 31197, A
2	38.8	6.7	38187	6	US-0-857-260-31	Sequence 31, App
3	38.4	6.7	12816	6	US-1-50-935-151	Sequence 15, App
4	38	6.6	15130	6	US-0-519-335-37	Sequence 37, App
5	37.6	6.5	435	6	US-0-953-349-35785	Sequence 35785, A
6	37	6.4	1214	6	US-10-953-349-34664	Sequence 34664, A
7	35.8	6.2	2246	7	US-1-293-697-1477	Sequence 1477, A
8	35.6	6.2	1951	6	US-10-953-349-29733	Sequence 29733, A
9	35.6	6.2	11918	7	US-1-1-257-8514-63	Sequence 63, App
10	35.6	6.2	37416	7	US-1-1-297-134-28	Sequence 28, App
11	35.4	6.2	4004	7	US-1-1-293-697-590	Sequence 590, App
12	35.2	6.1	3039	7	US-1-1-293-697-1476	Sequence 1476, A
13	35	6.1	945	6	US-0-953-349-23294	Sequence 23294, A
14	34.8	6.1	1116	6	US-10-953-349-25725	Sequence 25725, A
15	34	5.9	1633	6	US-10-953-349-38422	Sequence 38422, A
16	34	5.9	1797	7	US-1-1-293-697-885	Sequence 1885, A
17	33.8	5.9	464	6	US-10-953-349-25482	Sequence 25482, A
18	33.6	5.8	22118	7	US-1-1-284-877-16	Sequence 16, App
19	33	5.7	1773	6	US-0-953-349-32064	Sequence 32064, A
20	32.8	5.7	2845	7	US-1-1-293-697-1481	Sequence 1481, A
21	32.6	5.7	135	6	US-10-488-619-2301	Sequence 2301, App
22	32.6	5.7	696	6	US-10-953-349-37022	Sequence 37022, A
23	32.6	5.7	2114	6	US-10-953-349-2708	Sequence 2708, A
24	32.6	5.7	2537	7	US-1-1-293-697-2092	Sequence 2092, A
25	32.6	5.7	1129	6	US-10-953-349-21614	Sequence 21614, A

		ALIGNMENTS	
26	32.2	5.6	Sequence 31008, A
27	32.2	5.6	Sequence 38692, A
28	32	5.6	Sequence 38693, A
29	31.8	5.5	Sequence 35793, A
30	31.8	5.5	Sequence 26522, A
31	31.8	5.5	Sequence 32282, A
32	31.8	5.5	Sequence 390, App
33	31.8	5.5	Sequence 1893, App
34	31.8	5.5	GENERAL INFORMATION
35	31.6	5.5	Sequence 38, App1
36	31.6	5.5	Sequence 3584, A
37	31.6	5.5	Sequence 23308, A
38	31.6	5.5	Sequence 33324, A
39	31.6	5.5	Sequence 611, App
40	31.6	5.5	Sequence 1797, App
41	31.4	5.5	Sequence 24731, A
42	31.4	5.5	Sequence 21053, A
43	31.4	5.5	Sequence 516, App
44	31.2	5.4	Sequence 2896, A
45		5.4	Sequence 15679, A

Result No.	Score	Query Match	Length	DB	ID	Description
1	545	100.0	171823	10	HRV507799	AJ507799 Human her V01555 Epstein-Bar M80517 Epstein-Bar AY961628 Human her AJ41532 Human her AJ41533 Human her AJ414534 Human her AJ414535 Human her AY037858 Cercopith C0850504 Sequence AK127652 Homo sapi AF429315 Homo sapi Y00835 Epstein-Bar AX930675 Sequence AY037858 Cercopith C0850504 Sequence AK127652 Homo sapi Y00835 Epstein-Bar AX930675 Sequence C0774555 Sequence C0794832 Sequence C0881165 Sequence CQ891130 Sequence
2	545	100.0	172281	10	EBV	
3	543.4	99.7	184113	10	HS4B95RAJ	
4	543.4	99.7	171657	10	AY961628	
5	410.8	75.4	426	10	HRB414532	
6	410.8	75.4	426	10	HRB414533	
7	397.2	72.9	425	10	HRB414534	
8	397.2	72.9	425	10	HRB414535	
9	110.6	20.3	171096	10	AY037858	
10	110.6	13.8	2035	2	CQ850504	
11	110.6	13.8	2035	5	AK127652	
12	50.4	9.2	125020	5	AF429315	
13	48	8.8	2026	10	EBVTERM	
14	45.4	8.3	50	2	AF429315	
15	45.4	8.3	50	2	CQ774555	
16	45.4	8.3	50	2	C0794832	
17	45.4	8.3	50	2	C0881165	
18	45.4	8.3	50	2	CQ891130	

age 1

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OM nucleic search, using SW model

Run on: June 6, 2006, 17:26:38 ; Search time 410.696 Seconds
(without alignments)
9252.273 Million cell updates/sec

Title: US-10-6368-160-2
Perfect score: 545
Sequence: 1 cgccaaactcgccaaatg.....cattccaggccggtttgc 545

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%

ALIGNMENTS

IMMARTES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	545	100.0	545	12	AD043141	Ado3141 Epstein-Barr
2	545	100.0	172281	12	ADN12161	Adn12161 Epstein-Barr
3	110.6	20.3	171096	13	ADT05874	Adt05874 Cercopith
4	75	13.8	2035	13	ADR07467	Adr07467 Long lense
5	45.4	8.3	50	8	ABZ77478	Abz77478 Oligonucle
6	45.4	8.3	50	8	ACC83339	Acc83339 TP1 promo
7	45.4	8.3	50	8	ABZ81622	Abz81622 TP1 promo
8	45.4	8.3	50	9	ACC78948	Acc78948 TP1 promo
9	45.4	8.3	50	9	ACC78949	Acc78949 TP1 promo
10	45.4	8.3	50	10	ACF58279	Acf58279 Oligo use
11	45.4	8.3	50	10	ADH39824	Adh39824 TP1 promoter
12	45.4	8.3	50	12	ADJ45001	Adj45001 TP1 promoter
13	45.4	8.3	50	12	ADL73003	Adl73003 Notch sig
14	45.4	8.3	50	12	ADQ14415	Adq14415 TP1 promoter
15	45.4	8.3	50	13	ADS52104	Ads52104 Notch sig
16	44	8.1	50	8	ACCT83340	Acc83340 TP1 promo
17	44	8.1	50	10	ACF58280	Acf58280 Oligo use
C 18	44	8.1	50	12	ADP22004	Adp22004 Notch sig

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGMENTS

AD043141 13141 ADO43141 Standard; DNA; 545 BP.
AD043141;

12-AUG-2004 (first entry)
Epstein-Barr virus LMP2A promoter.
Epstein-Barr virus; LMP2A; promoter; adenovirus; vector; gene therapy;
cytostatic; ds.

Human herpesvirus 4.

WO2004042025-A2.
21-MAY-2004.
3-0-OCT-2003; 2003WO-US034858.
01-NOV-2002; 2002US-0423203P.
(CELL-) CELL GENESYS INC.

Yu DC, Ramesh N;
WPI; 2004-390609/36.

Claim 7: SEQ ID NO 2; 36pp; English.

New replication-competent adenovirus vector comprising an adenovirus genome for replication, useful as a vehicle for introducing new genetic capability.

The present sequence is the Epstein-Barr virus (EBV) LMP2A gene promoter region. The LMP2 gene encodes 2 distinct proteins, LMP2A and LMP2B. LMP2 aggregates in patches within the plasma membrane of latently infected B-lymphocytes. The consistent expression of LMP2A in Hodgkin's disease and nasopharyngeal carcinoma suggests an important function for this protein in oncogenesis. The invention provides replicant-competent adenovirus

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 6, 2006, 17:52:13 ; Search time 3685.56 Seconds
(without alignments)
8269.032 Million cell updates/sec

Title: US-10-698-160-2

Perfect score: 545

Sequence: 1 cgccaccaactgcggcaatg.....cattcaggccggtttgcga 545

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0‡
Maximum Match 100‡
Listing first 45 summaries

Database : EST:
EST:
1: gb_est1:
2: gb_est3:
3: gb_est4:
4: gb_est5:
5: gb_est6:
6: gb_hnc:
7: gb_est2:
8: gb_est7:
9: gb_est8:
10: gb_est9:
11: gb_gss1:
12: gb_gss2:
13: gb_gss3:
14: gb_gss4:
.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1		75	13.8	587	9	DA645119	DA645119
2		49	9.0	524	9	DA644493	DA644493
c 3		44	8.1	1359	4	CA472883	AGENCOURT
c 4		43.8	8.0	939	14	CNS00CNG	AL059400 Drosophil
c 5		42.4	7.8	823	14	AG106932	AG106932 Pan trogl
c 6		40.8	7.5	780	14	DR890143	1471125 M
c 7		40.4	7.4	1079	12	CC266659	CC266659 CH261-97G
c 8		39.8	7.3	375	12	CB082035	CB082035 tigr-988-
c 9		39.6	7.3	588	11	AQ531217	AQ531217 RPC-11-3
c 10		39.4	7.2	294	4	CB852782	CB852782 UI-CP-FN0
c 11		39.4	7.2	650	14	AG536872	AG536872 Mus muscu
c 12		39.4	7.2	661	9	DR112573	DR112573 RTS1 29 D
c 13		39.4	7.2	692	14	CNS0057WH	AL050923 Drosophil
c 14		39.2	7.2	405	2	BJ306689	BJ306689
c 15		39.2	7.2	1101	10	AG898391	AG898391 Oryza sat
c 16		38.8	7.1	966	14	DR91511	DR91511 147661 M
c 17		38.6	7.1	784	10	AQ389558	AQ389558 RPC11-15
c 18		38.4	7.0	352	11	CNS0166K	AL106358 Drosophil
c 19		38.0	7.0	1225	14		

ALIGNMENTS

RESULT 1	LOCUS	DA645119	587 bp mRNA	LINEAR EST 08-NOV-2005
DEFINITION	DA645119 LYMPB2 Homo sapiens cDNA clone LYMPC2002236 5', mRNA			
SEQUENCE				
ACCESSION	DA645119			
VERSION	DA645119.1			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euchondrocytes; Mammalia; Homo; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 587)			
AUTHORS	Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T., and Sugano,S.			
COMMENT	1 (bases 1 to 587)			
JOURNAL	Genome Res. 16 (1), 55-65 (2006)			
PUBLMED	1634450			
COMMENT	Contact: Takao Isogai FLJ Project (FLJ Team) Helix Research Institute 2-6-7 Kazusa-Kamatai, Kisarazu, Chiba, 292-0818, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: flj-cdna@nifty.com			
FEATURES	Location/Qualifiers			
source	1. .587 /organism="Homo sapiens" /mol_type="mRNA"			

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OM nucleic - nucleic search, using sw model

Run on: June 6, 2006, 18:05:44 ; Search time 145.496 Seconds
(without alignments)

Title: US-10-698-160-2

Perfect score: 545

Sequence: 1 cgaccaactggggcaatg.....cattcaggccgttttgc a 545

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : Issued Patents NA:*

1: /EMC_Celerra_SIDS3/prodata/2/1naa/1/COMB.seq:*

2: /EMC_Celerra_SIDS3/prodata/2/1na/5_-COMB.seq:*

3: /EMC_Celerra_SIDS3/prodata/2/1na/6A_COMB.seq:*

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7: /EMC_Celerra_SIDS3/prodata/2/1na/PCUTUS_COMB.seq:*

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10: /EMC_Celerra_SIDS3/prodata/2/1na/bäckfile1.seq:*

RESULT 1
US-08-232-463-14/C
Sequence 14, Application US/08232463
Parent No. 5670367

GENERAL INFORMATION:

APPLICANT: DORNER, F. P.

APPLICANT: SCHEIFLINGER, F.

APPLICANT: FALKNER, F. G.

TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEES: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0399

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/232,463

APPLICATION NUMBER: US/08/232,463

FILING DATE: 25-AUG-1991

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 313

APPLICATION NUMBER: US/07/935,313

FILING DATE:

APPLICATION NUMBER: EP 91 114 300.6

FILING DATE: 25-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 30472/114 IMMU

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-9300

TELEFAX: (703) 683-4109

TELEX: 899149

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 7218 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	39.6	7.3	7218	2 US-08-232-463-14	Sequence 14, Appl
c 2	36.2	6.6	3635	3 US-09-312-762A-6	Sequence 6, Appl
c 3	36.6	6.6	15003	3 US-09-949-016-12319	Sequence 1319, A
c 4	36.6	6.6	15004	3 US-09-949-016-15658	Sequence 15658, A
c 5	34.8	6.4	11366	3 US-09-949-016-13616	Sequence 13616, A
c 6	34.6	6.3	44377	3 US-09-949-016-11840	Sequence 11840, A
c 7	34.6	6.3	44378	3 US-09-949-016-15969	Sequence 15969, A
c 8	33.8	6.2	35337	3 US-09-949-016-17249	Sequence 17249, A
c 9	33.8	6.2	40548	3 US-09-949-016-13317	Sequence 13317, A
c 10	33.8	6.2	40517	3 US-09-949-016-15197	Sequence 15197, A
c 11	32.8	6.0	474	3 US-09-949-016-11033	Sequence 18033, A
c 12	32.8	6.0	24384	3 US-09-949-016-14950	Sequence 14950, A
c 13	32.8	6.0	63860	3 US-09-949-016-15825	Sequence 15825, A
c 14	32.8	6.0	99304	3 US-09-949-016-15440	Sequence 15440, A
c 15	32.8	6.0	422592	3 US-09-949-016-11812	Sequence 1882, A
c 16	32.6	6.0	1185	4 US-09-949-016-14514	Sequence 4514, AP
c 17	32.4	5.9	601	3 US-09-949-016-14447	Sequence 144470, A
c 18	32.2	5.9	11880	3 US-09-949-016-15203	Sequence 15203, A
c 19	32.2	5.9	11280	3 US-09-949-016-15204	Sequence 15204, A
c 20	32.2	5.9	43391	5 US-09-948-016-429-252	Sequence 252, APP
c 21	32.2	5.9	44554	3 US-09-949-016-12787	Sequence 1287, A
c 22	32.2	5.9	44555	3 US-09-949-016-12043	Sequence 12043, A
c 23	32.2	5.9	199345	3 US-09-949-016-15436	Sequence 15436, A

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OM nucleic - nucleic search, using SW mode!

Run on: June 6, 2006, 18:14:24 ; Search time 1061.29 Seconds
(without alignments)

Title: US-10-698-160-2

Perfect score: 545

Sequence: 1 cgccaccaactggccaaatg.....cattccaggccgggtttgca 545

Scoring table: IDENTITY_NUC

GAP0 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 0

Post-processing: Maximum Match 10⁴

Listing first 45 summaries

Published Applications NA Main:
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 2: /EMC Celerra_SIDS3_ptoda2/pubnra/US08_pubcomb_seq:
 3: /EMC Celerra_SIDS3_ptoda2/pubnra/US09_pubcomb_seq:
 4: /EMC Celerra_SIDS3_ptoda2/pubnra/US09B_pubcomb_seq:
 5: /EMC Celerra_SIDS3_ptoda2/pubnra/US09C_pubcomb_seq:
 Database :

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13: /EMC_Celerra_SIDS3/.ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/.ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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SUMMARIES

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1	545	100.0	545	8	US-10-698-160-2		Sequence 2, Appli
C	2	473.6	66.9	612	6	US-10-027-632-180450	Sequence 180450,
C	3	471.6	86.9	612	7	US-10-027-332-180450	Sequence 180450,
C	4	110.6	20.3	171096	9	US-10-612-869-8	Sequence 8, Appli
	5	45.4	8.3	50	9	US-10-763-362-22	Sequence 22, Appli
	6	45.4	8.3	50	9	US-10-812-44-5	Sequence 5, Appli
	7	45.4	8.3	50	9	US-10-765-727-34	Sequence 34, Appli
	8	45.4	8.3	50	9	US-10-846-989-68	Sequence 68, Appli
	9	45.4	8.3	50	10	US-10-764-415B-11	Sequence 11, Appli
	10	45.4	8.3	50	10	US-10-845-834-12	Sequence 12, Appli
	11	45.4	8.3	50	10	US-10-958-784-22	Sequence 22, Appli
	12	45.4	8.3	50	15	US-11-078-735-46	Sequence 46, Appli
	13	41.4	8.3	50	16	US-11-050-346-44	Sequence 44, Appli
	14	44	8.1	50	9	US-10-763-362-23	Sequence 23, Appli
C	15	44	8.1	50	9	US-10-812-144-6	Sequence 6, Appli
C	16	44	8.1	50	9	US-10-846-989-35	Sequence 35, Appli
C	17	44	8.1	50	9	US-10-846-989-35	Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-10-698-160-2
; Sequence 2, Application US/10698160
; Publication No. US20040171159A1
; GENERAL INFORMATION:
; APPLICANT: DC Yu
; APPLICANT: Nagarajan Ramesh
; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTOR
; TITLE OF INVENTION: COMPRISING EBV-SPECIFIC PROMOTER
; FILE REFERENCE: CELL-033
; CURRENT APPLICATION NUMBER: US/10/698,160
; CURRENT FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: 60/442,203
; PRIOR FILING DATE: 2003-11-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SBQ ID NO: 2

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OM nucleic - nucleic search, using bw model

Run on: June 6, 2006, 18:40:59 ; Search time 36.0089 Seconds (without alignments)

1782.525 Million cell updates/sec

Title: US-10-698-160-2

Perfect Score: 545

Sequence: 1 cgcaaccactgcggcaatg.....cattcagggcggttttgc a 545

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 246837 seqs, 58886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New.*

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2: /EMC_Celerra_SIDS3/prodata/2/pubnpna/US06_NEW_PUB.seq;*

3: /EMC_Celerra_SIDS3/prodata/2/pubnpna/US07_NEW_PUB.seq;*

4: /EMC_Celerra_SIDS3/prodata/2/pubnpna/US08_NEW_PUB.seq;*

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8: /EMC_Celerra_SIDS3/prodata/2/pubnpna/US60_NEW_PUB.seq;*

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

RESULT 1
US-11-217-529-77277/c

; Sequence 77277, Application US/11217529
; Publication No. US2006009612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOHIKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 77277
; LENGTH: 666
; ORGANISM: *Saccharomyces pastorianus*

RESULT 2
US-11-293-697-382/c

; Sequence 382, Application US/11293697
; Publication No. US2006010576A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05

Summary

Result No.	Query	Match	Length	DB ID	Description
c 1	30.6	5.6	666	7 US-11-217-529-77277	Sequence 77277, A
c 2	30.6	5.6	1808	6 US-11-293-697-382	Sequence 382, APP
c 3	30.6	5.6	2745	7 US-11-293-697-440	Sequence 440, APP
c 4	30.2	5.5	4239	6 US-10-511-937-543	Sequence 543, APP
c 5	30.0	5.5	1370	6 US-10-953-349-34135	Sequence 40063, A
c 6	29.4	5.4	2516	6 US-10-953-349-40063	Sequence 34135, A
c 7	28.6	5.2	2448	7 US-11-217-529-3847	Sequence 3847, AP
c 8	28.4	5.2	1104	6 US-10-953-349-702	Sequence 8702, AP
c 9	28.4	5.2	123361	6 US-10-505-928-151	Sequence 151, APP
c 10	28.2	5.2	959	6 US-10-953-349-28855	Sequence 28855, A
c 11	28.2	5.2	1050	6 US-10-953-349-10035	Sequence 10035, A
c 12	28.2	5.2	1235	6 US-10-953-349-16361	Sequence 16861, A
c 13	28.2	5.2	1766	6 US-10-505-928-614	Sequence 614, APP
c 14	28.2	5.2	2145	7 US-11-293-697-9	Sequence 9, APP
c 15	28	5.1	849	6 US-10-505-349-34426	Sequence 34426, A
c 16	28	5.1	1706	6 US-10-505-928-762	Sequence 762, APP
c 17	28	5.1	2786	6 US-10-196-749-307	Sequence 307, APP
c 18	27.8	5.1	1624	6 US-10-503-349-32219	Sequence 32219, A
c 19	27.6	5.1	958	6 US-10-503-349-359887	Sequence 359887, A
c 20	27.6	5.1	3124	7 US-11-293-697-568	Sequence 568, APP
c 21	27.6	5.1	3333	7 US-11-217-529-232	Sequence 232, APP
c 22	27.4	5.0	584	6 US-10-488-639-1411	Sequence 1431, APP
c 23	27.4	5.0	1023	7 US-11-145-307A-177	Sequence 177, APP
c 24	27.4	5.0	1960	7 US-11-293-697-1665	Sequence 1665, APP
c 25	27.4	5.0	2290	7 US-11-293-697-191	Sequence 191, APP

FOR OFFICIAL USE ONLY

ACCESS DB #

191632

PLEASE PRINT CLEARLY

Scientific and Technical Information Center

CRPE

SEARCH REQUEST FORM

Requester's Full Name: DAVID GUZO Examiner #: 70677 Date: 6/1/06
Art Unit: 1636 Phone Number: 2-0767 Serial Number: 10/698160
Location (Bldg/Room#): 2079 (Mailbox #): 2070 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Date: _____

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please run a regular plus interphase sequence search on SEQ ID NO: 1 and 2.

1 - 575 Nt
2 - 545
Thanks